

WO 00/00606

PCT/AU99/00523

FIG	GURE	1	1/4	**	ē					
Human neuropeptide Y - Y7 sequençe alignment										
hy1p hy2p hy7p	.1 1 1	, ,	MNS	T L F S Q V E N H S V H S VEEMKVEQ Y G P Q T S E N W H P I W N V N D T	16 26 25					
hy1p hy2p hy7p	17 27 26	N F S E K N A Q L L A F E N D T P R G E L V P D P E P E L I K H H L Y S D I N I T Y V N Y	IDIS T K I I CIN		52 62 60					
hy1p hy2p hy7p	53 63 61	LGVSGNLALIIIIILK LGVIGNSLVIHVVIK LCMMGNTVVCFIVMR	IFIKISIMRTVT	NIFIELLANDAVADATA	88 98 96					
hy1p hy2p hy7p	89 99 97	VAIMCLPFTFVYTLM VNTLCLPFTLTYTLM VGIFGMPITLLDNII	IC FIMIK MICIP V	LIGILIANDIV MAGIL MAI	124 134 132					
hy1p hy2p hy7p	125 135 133	TVSIESLYLIAVERH QVSTITLTVIALDRH AASVETLYAIAVDRF	QLIINPRG RCIVYHLE QCVVYPFK	WRPNNRHAYVGIA SKISKRISFLIIG PKLTIKTAFVIIM	160 170 168					
hy1p hy2p hy7p	161 171 169	VIWVLAVASSLPFLI LAWGISALLASPLAI IIWVLAITIMSPSAV		MAREACIMILE I I DUC	193 198 204					
hy1p hy2p hy7p	194 199 2 05	DKYVCFDQFPSDSHR EIVACTEKWPGEEKS PVYWCREDWPNQEMR	I Y GITIV Y SIII	SSILIIMVIDAGI	226 234 237					
hy1p hy2p hy7p	227 235 238	IFICYFKIYIRLKRR ISFSYTRIWSKLKNH IVIMYGRIGISLFRA	VSIPI - IGIA AI	MIDH VHO BIBIO KTIT KI	259 268 273					
hy1p hy2p hy7p	260 269 274	RINIMLLS IVVAFAV MLVCVVVVFAV KII KMLLIVALLEI L	SWI PIIH AIFI		293 298 309					
hy1p hy2p hy7p	294 299 310	ATCNHNULFLLCHLT DLKEYKLIFTVFHII LQIINIYIYPFAHWL	AMCISTIF AIN	PILLIVEWMNISHIVER	329 334 345					
hy1p hy2p hy7p	330 335 346	DLQFFFNFCDFRSRD AFLSAFRCEQRLDAI GFQEAFQLQLCQKRA	DDYETIAM HSEVSVTF KPMEAYTL	STMHTDVSKTSLK KAKKNLEVRKNSG KAKSHVLINTSNQ	365 370 381					
hy1p hy2p hy7p	366 371 382	QASPVAFKKINNNDD PNDSFTEATNV LVQESTFQNPHGETL		PNRN	384 381 408					



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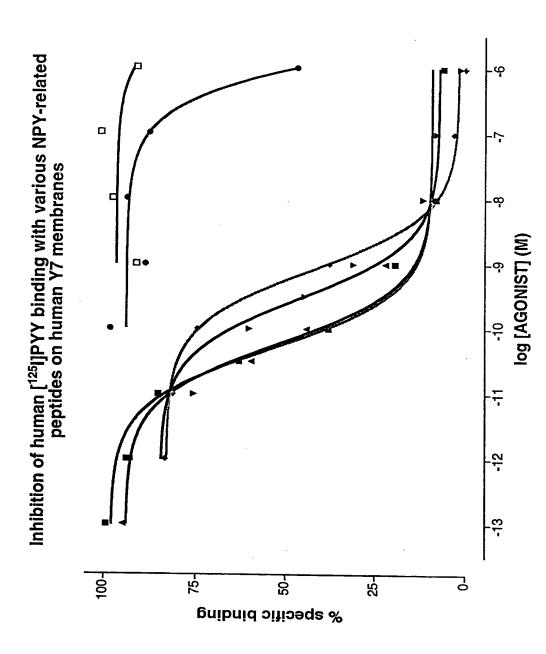
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[125I]PYY (50pM)



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FIGURE 3

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Mouse NPY-Y7 Gene

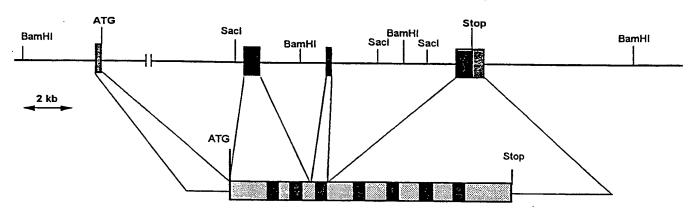


FIGURE 4

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Human-Mouse NPY Y7 Receptor Alignment

hy7 mY7	1	M F M S	IMN TMS	E KV	VD TN	188E 188E	NWH SWN	H P I V	NN V S G	T D V	кн н он н	L YSI	N I C	I T Y V I T Y V	38 38
hy7 mY7	39 39	N Y N Y	Y L F	Q P (A A V <u>A</u> A	VF I	IS Y	FL LL	F V	LCM	MGN VGN	T V V 0	OF IN	VMRN VIRN	76 76
hy7 mY7	77 77	KH RH	МН Т Т Н М	1 T V 1 T V	N F L I	L N L L N L	AIS AIS	DLI	.VG VG	I F C	MPI MPI	T	I N C	I AGW I AGW	114 114
hy7 mY7	115 115	P F	GN T GS S	MC I	(180 (180	ELVC	G I S	V A A	AS V	FTL FTL	VAI.	A V D I A V D I	RFQC	2 V V Y 2 V V Y	152 152
hy7 mY7	153 153	P F	KPK KPK	L T L T	KT A	\	I M I	I W \	LA LA	I T I I A I	MSP: MTP:	5 A VI 5 A I I	MLH \	VQEE VQEE	190 190
hy7 mY7	191 191	K Y K Y	YRV YRV	RLI RLS	NS QN	KTS KTS	PVY TVY	WC F	RED\ RED\	VPN VPR	QEM HEM	RKI RRI	Y T T \ Y T T \	VLFA VLFA	228 228
hy7 mY7	229 229	N I	YLA YLA	PLS	SLIV SLIV	/	GRI ARI	G I S	S L F	R AA K TA	V P H A H C	TGRI	KNOE	EQWH RPVQ	266 264
hy7 mY7	267 265	C M	SRK	KQ I KQ I		KM L L KM L L	I V A	\ L L F	1 L 3	SWL SWL	P L W P L W	T L MN T L MN	MLSE MLSE	DYAD DYTD	304 302
hy7 mY7	305 303	L S L S	PN E	L Q L R	INI	Y 1 Y Y 1 Y	/PFA	HWL	A F (BNS BNS	S V N	P '	YGF I YGF I	NEN NEN	342 340
hy7 mY7	343 341	F R	RG F NG F	Q E/	AFQL AFQI	Q L C	QK QK K	AKI	ME.	A Y T A Y S	L KA L RA	KSHY KRN	V L I I I V I I	NTSN NTSG	380 376
hy7 mY7	381 377	Q L L	VQE VQE	STE	QN F	HG E	TL L NLG	YR CG	(S A (S A I	EN P ON P	NRN HRN	P			408 405